


```

gtggggacat gtgtgtcaga gggaagctac cctgcagga ctcttagctg gcaattggat 480
gggaagcccc tgggtgcctaa tgagaaggga gtatctgtga aggaacagac caggagacac 540
cctgagacag ggctcttcac actgcagtcg gagctaattg tgacccagc ccggggagga 600
gatccccgtc ccaccttctc ctgtagcttc agcccaggcc ttccccgaca ccgggccttg 660
cgcacagccc ccatccagcc ccgtgtctgg gagcctgtgc ctctggagga ggtccaattg 720
gtggtggagc cagaagggtg agcagtagct cctggtggaa ccgtaaccct gacctgtgaa 780
gtccctgccc agccctctcc tcaaatccac tggatgaagg atggtgtgcc cttgcccctt 840
ccccccagcc ctgtgctgat cctccctgag atagggcctc aggaccaggg aacctacagc 900
tgtgtggcca ccattccag ccacgggccc caggaaagcc gtgctgtcag catcagcatc 960
atcgaaccag gcgaggagg gccaactgca ggctctgtgg gaggatcagg gctgggaact 1020
ctagccctgg ccctggggat cctgggaggc ctggggacag ccgccctgct cattggggtc 1080
atcttgtggc aaaggcggca acgccgagga gaggagagga agggcccaga aaaccaggag 1140
gaagaggagg agcgtgcaga actgaatcag tcggaggaac ctgaggcagg cgagagtagt 1200
actggagggc cttgaggggc ccacagacag atcccatcca tcagctccct tttctttttc 1260
ccttgaactg ttctggcctc agaccaactc tctcctgtat aatctctctc ctgtataacc 1320
ccaccttgcc aagctttctt ctacaaccag agccccccac aatgatgatt aaacacctga 1380
cacatcttgc a 1391

```

<210> 2

<211> 1020

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1020)

<223>

<400> 2

```

atg gca gcc gga aca gca gtt gga gcc tgg gtg ctg gtc ctc agt ctg 48

```

Met	Ala	Ala	Gly	Thr	Ala	Val	Gly	Ala	Trp	Val	Leu	Val	Leu	Ser	Leu		
1				5					10					15			
tgg	ggg	gca	gta	gta	ggt	gct	caa	aac	atc	aca	gcc	cgg	att	ggc	gag		96
Trp	Gly	Ala	Val	Val	Gly	Ala	Gln	Asn	Ile	Thr	Ala	Arg	Ile	Gly	Glu		
			20					25					30				
cca	ctg	gtg	ctg	aag	tgt	aag	ggg	gcc	ccc	aag	aaa	cca	ccc	cag	cgg		144
Pro	Leu	Val	Leu	Lys	Cys	Lys	Gly	Ala	Pro	Lys	Lys	Pro	Pro	Gln	Arg		
			35				40					45					
ctg	gaa	tgg	aaa	ctg	aac	aca	ggc	cgg	aca	gaa	gct	tgg	aag	gtc	ctg		192
Leu	Glu	Trp	Lys	Leu	Asn	Thr	Gly	Arg	Thr	Glu	Ala	Trp	Lys	Val	Leu		
	50					55					60						
tct	ccc	cag	gga	gga	ggc	ccc	tgg	gac	agt	gtg	gct	cgt	gtc	ctt	ccc		240
Ser	Pro	Gln	Gly	Gly	Gly	Pro	Trp	Asp	Ser	Val	Ala	Arg	Val	Leu	Pro		
65					70				75					80			
aac	ggc	tcc	ctc	ttc	ctt	ccg	gct	gtc	ggg	atc	cag	gat	gag	ggg	att		288
Asn	Gly	Ser	Leu	Phe	Leu	Pro	Ala	Val	Gly	Ile	Gln	Asp	Glu	Gly	Ile		
				85					90					95			
ttc	cgg	tgc	cag	gca	atg	aac	agg	aat	gga	aag	gag	acc	aag	tcc	aac		336
Phe	Arg	Cys	Gln	Ala	Met	Asn	Arg	Asn	Gly	Lys	Glu	Thr	Lys	Ser	Asn		
			100					105					110				
tac	cga	gtc	cgt	gtc	tac	cag	att	cct	ggg	aag	cca	gaa	att	gta	gat		384
Tyr	Arg	Val	Arg	Val	Tyr	Gln	Ile	Pro	Gly	Lys	Pro	Glu	Ile	Val	Asp		
		115					120					125					
tct	gcc	tct	gaa	ctc	acg	gct	ggt	gtt	ccc	aat	aag	gtg	ggg	aca	tgt		432
Ser	Ala	Ser	Glu	Leu	Thr	Ala	Gly	Val	Pro	Asn	Lys	Val	Gly	Thr	Cys		
	130					135					140						
gtg	tca	gag	gga	agc	tac	cct	gca	ggg	act	ctt	agc	tgg	cac	ttg	gat		480
Val	Ser	Glu	Gly	Ser	Tyr	Pro	Ala	Gly	Thr	Leu	Ser	Trp	His	Leu	Asp		
145					150				155					160			
ggg	aag	ccc	ctg	gtg	cct	aat	gag	aag	gga	gta	tct	gtg	aag	gaa	cag		528
Gly	Lys	Pro	Leu	Val	Pro	Asn	Glu	Lys	Gly	Val	Ser	Val	Lys	Glu	Gln		
				165				170						175			
acc	agg	aga	cac	cct	gag	aca	ggg	ctc	ttc	aca	ctg	cag	tcg	gag	cta		576
Thr	Arg	Arg	His	Pro	Glu	Thr	Gly	Leu	Phe	Thr	Leu	Gln	Ser	Glu	Leu		
			180					185					190				
atg	gtg	acc	cca	gcc	cgg	gga	gga	gat	ccc	cgt	ccc	acc	ttc	tcc	tgt		624
Met	Val	Thr	Pro	Ala	Arg	Gly	Gly	Asp	Pro	Arg	Pro	Thr	Phe	Ser	Cys		
			195				200					205					
agc	ttc	agc	cca	ggc	ctt	ccc	cga	cac	cgg	gcc	ttg	cgc	aca	gcc	ccc		672
Ser	Phe	Ser	Pro	Gly	Leu	Pro	Arg	His	Arg	Ala	Leu	Arg	Thr	Ala	Pro		
	210					215					220						
atc	cag	ccc	cgt	gtc	tgg	gag	cct	gtg	cct	ctg	gag	gag	gtc	caa	ttg		720
Ile	Gln	Pro	Arg	Val	Trp	Glu	Pro	Val	Pro	Leu	Glu	Glu	Val	Gln	Leu		
225					230					235					240		

Met	Ala	Ala	Gly	Thr	Ala	Val	Gly	Ala	Trp	Val	Leu	Val	Leu	Ser	Leu
1				5					10					15	
Trp	Gly	Ala	Val	Val	Gly	Ala	Gln	Asn	Ile	Thr	Ala	Arg	Ile	Gly	Glu
			20					25					30		
Pro	Leu	Val	Leu	Lys	Cys	Lys	Gly	Ala	Pro	Lys	Lys	Pro	Pro	Gln	Arg
		35					40					45			
Leu	Glu	Trp	Lys	Leu	Asn	Thr	Gly	Arg	Thr	Glu	Ala	Trp	Lys	Val	Leu
	50					55					60				

His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser Ile
 305 310 315 320

Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly Ser
 325 330 335

Gly Leu Val

<210> 4

<211> 336

<212> DNA

<213> Homo sapiens

<400> 4

gctcaaaaca tcacagcccg gattggcgag ccaactggtgc tgaagtgtaa gggggccccc 60
 aagaaaccac cccagcggct ggaatggaaa ctgaacacag gccggacaga agcttggaag 120
 gtctgtcttc cccagggagg aggcccttg gacagtgtgg ctctgtctct tcccaacggc 180
 tccctcttcc ttccggctgt cgggatccag gatgagggga ttttccggtg ccaggcaatg 240
 aacaggaatg gaaaggagac caagtccaac taccgagtcc gtgtctacca gattcctggg 300
 aagccagaaa ttgtagattc tgcctctgaa ctcacg 336

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 5

aaccatctcg caaataaata 20

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 6

acgcacagaa tctagcgctt

20

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 7

ctcccttctc attaggcacc

20

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 8

tggggacatg tgtgtcagag

20

<210> 9

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 9

acgacggaat tctgcagata tcatggcagc cggaacagca gttggagcc

49

<210> 10

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 10

acgacggaat tccaccacac tggactagt g

31